11th GERMPLASM & BREEDING

8th MOLECULAR BIOLOGY

ISSCT WORKSHOP

Saint-Gilles Réunion Island / 1–5 June 2015



« Pushing the frontiers of sugarcane improvement »

ABSTRACT

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ORGANIZATION

SUMMARY

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FLUORESCENCE *IN SITU* HYBRIDIZATION IN SUGARCANE OR FISH-ING IN THE GENOMIC WILDERNESS

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Keywords: Cytogenetics, FISH BAC sugarcane

Cytogenetics applied to sugarcane has brought our fundamental understanding of the sugarcane genome to a new level. In the mid-nineties, Genomic in situ Hybridisation (GISH) was first applied to sugarcane to determine the specific composition of the modern cultivar R570. GISH revealed the chromosomal composition of R570 was 80% *Saccharum officinarum*, 10% *S. spontaneum* and 10% of recombined chromosomes. The Australian counterpart Q165, revealed a slightly different species composition as 75%, 15% and 10%, respectively. Both R570 and Q165 genetic maps have portrayed a partial coverage of linkage groups (LG) despite the large number of molecular markers invested in the maps. It also shows that *S. spontaneum* chromosomes seem to have a better vertical coverage than *S. officinarum* chromosomes as the *S. spontaneum* genome is more polymorphic. To gain a better understanding of the genome composition in terms of LG number per homology group (HG) and species attribution of the LG, we applied BAC-FISH to sugarcane. Bacterial Artificial Chromosomes (BAC) consist of large chromosome segments (around 100kb). BAC from the *Sorghum* or *Saccharum* genomes were used as anchorage points on the sugarcane cultivars to identify homologous/homeologous chromosomes for each HG. We will present some examples of results of BAC-FISH applied to several cultivars for at least 4 different HG. The determination and comparison of the number of chromosomes per HG to the number of LG from the genetic maps will determine the saturation level of the genetic maps. This will help us to obtain critical knowledge of the horizontal chromosome distribution for a particular cultivar and compare its structure to another cultivar. Eventually we will have a better understanding of the distribution of the chromosomes during crossing and this will help breeders to make more informed and targeted choices in their selection programs.